What is claimed is:

1.   A method for indexing a population, comprising determining products of the reaction of a population to be indexed with each of a plurality of different indexing reagents, wherein

     each reaction product is indicative of a different cognate sub-population of individuals,

     the population is indexed by the constituency of sub-populations thus determined;

     the reactions are conducted in homogeneous media, and

     the reaction products are determined in homogeneous media.

2.   A method for indexing a population, comprising determining products of the reaction of a population to be indexed with each of a plurality of different indexing reagents, wherein

     each reaction product is indicative of a different cognate sub-population of individuals,

     the population is indexed by the constituency of sub-populations thus determined;

     the reaction products are determined without physically separating determined products from the reactions.

3.   A method for indexing a population, comprising determining products of the reaction of a population to be indexed with each of a plurality of different indexing reagents, wherein

     each reaction product is indicative of a different cognate sub-population of individuals,

     the population is indexed by the constituency of sub-populations thus determined;

     the reactions are conducted in homogeneous media, and

     the reaction products are determined without physically separating determined products from the reactions.

4.   A method for indexing a population, comprising determining products of the reaction of a population to be indexed with each of a plurality of different indexing

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reagents, wherein

each reaction product is indicative of a different cognate sub-population of individuals,

the population is indexed by the constituency of sub-populations thus determined;

the reactions are conducted in homogeneous media;

the reaction products are determined in homogeneous media, and

the reaction products are determined without physically separating the determined products from the reactions.

5.   A method according to any of the foregoing numbered paragraphs wherein the reactions are determined over time and the resulting kinetic data is used to determine the reaction products.

6.   A method according to paragraph 5, wherein the reactions are monitored continuously.

7.   A method according to paragraph 5, wherein the reactions are monitored discontinuously.

8.   A method according to any of the foregoing numbered paragraphs, wherein reactions of two or more indexing reagents with the population are multiplexed together.

9.   A method according to any of the foregoing numbered paragraphs, wherein a substantial fraction of the possible sub-populations of a given type are thus determined.

10.   A method according to paragraph 9, wherein the substantial fraction is any of or range between any two of 25%, 30%, 35%, 40%, 45% 50%, 55%, 60%, 65%, 70%, 75%, 80%, 82%, 84%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or more than 99%.

11.   A method according to paragraph 9 or 10, wherein substantially all of the sub-population are determined.

12.   A method according to any of the foregoing numbered paragraphs, wherein the population is a population of polynucleotides and the sub-populations are sequence-specific sub-populations.

13.   A method according to paragraph 12, wherein sub-populations represents the expression of genes.

14.   A method according to -paragraph 12 or 13, wherein the population is a population of mRNAs.

15.   A method according to -paragraph 12 or 13, wherein the population is a representative of mRNAs.

16.   A method according to -paragraph 12 or 13, wherein the population is a population of cDNAs.

17.   A method according to any of the foregoing n ' umbered paragraphs, wherein the indexing reagents comprise sequence-specific indexing probes.

18.   A method according to paragraph 17, wherein the sequence specific probe is specific for a sequence n bases long, where n is 1, 2, 3, 4, 5, 6, 7 or 8.

19.   A method according to paragraph 18, wherein the sequence specific probe is specific for a sequence n bases long, where n is 1, 2, 3, 4, 5 or 6.

20.   A method according to paragraph 19, wherein the sequence specific probe is specific for a sequence n bases long, where n is 2, 3, 4 or 5.

21.   A method according to any of paragraphs 17 through 20, wherein the sequence-specific probe is n bases long, each different sequence possible for a sequence n bases long is specific for a sub-population to be determined, and indexing

reactions between the population and indexing reagents that comprise a substantial fraction of all the possible sequences n bases long are determined.

22. A method according to paragraph 9, wherein the substantial fraction is any of or range between any two of 25%, 30%, 35%, 40%, 45% 50%, 55%, 60%.,65%, 70%, 75%, 80%, 82%, 84%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or more than 99%.

23. A method according to paragraph 21, wherein substantially all of the sub-populations defined by the probe sequences are determined.

24. A method according to paragraph 21, wherein all of the sub-populations defined by the probe sequences are determined.

25. A method according to any of the foregoing numbered paragraphs, wherein the indexing reagents comprise amplification primers.

26. A method according to any of the foregoing numbered paragraphs, wherein the probes are stand-d is placement indexing adaptors.

27. A method according to paragraph 25, comprising:
(A) distributing strand-d is placement indexing adaptors into discrete containers;
(B) contacting each of the strand-d is placement indexing adaptors in the containers with an aliquot of a sample population of polynucleotides;
(C) carrying out strand-displacement indexing reactions between the sample polynucleotides and the indexing adaptors in each container;
(D) amplifying by PCR the polynucleotides that form strand-displaced structures with indexing adaptors in each container;
(E) quantifying the amount of amplified polynucleotide in each container, thereby determining the absence or the amount of cognate polynucleotides in the population, and
(F) indexing the population by the absence, the presence, and amount of sample polynucleotides cognate to the indexing adaptors in each of the containers,

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28.   A method according to paragraph 25, wherein the indexing sequ nce comprises a Type 11 restriction cite contiguous with a five nucleotide base-pair sequence.

29.   A device or set of devices for indexing a population, comprising a plurality indexing reagents disposed in a plurality of containers, wherein the indexing reagent in each container is specific for a cognate sub-population and the plurality of indexing reagents in the device comprises reagents specific for a substantial fraction of all the sub-populations of a given type that can be indexed in the population.

30.   A device according to paragraph 29, wherein the substantial fraction is any of or range between any two of 25%, 30%, 35%, 40%, 45% 50%, 55%, 60%, 65%, 70%, 75%, 80%, 82%, 84%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or more than 99%.

31.   A device according to paragraph 29, wherein substantially all of the sub-populations of the given type are determined.

32.   A device according to paragraph 29, wherein the containers are wells of one or more micro-titer plates.

33.   A device according to any of paragraphs 29-32, wherein the indexing reagents comprise sequence-specific indexing probes.

34.   A device according to paragraph 33, wherein the sequence specific probe is specific for a sequence n bases long, where n is 1, 2, 3, 4, 5, 6, 7 or 8.

35.   A device according to paragraph 32, wherein the sequence specific probe is specific for a sequence n bases long, where n is 1, 2, 3, 4, 5 or 6.

36.   A device according to paragraph 33, wherein the sequence specific probe is specific for a sequence n bases long, where n is 2, 3, 4 or 5.

37.   A device according to any of paragraphs 29 through 33, wherein the sequence-specific probe is n bases long, each different sequence possible for a sequence

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n bases long is specific for a sub-population to be determined, and the plurality of indexing reagents comprise indexing reagents with a substantial fraction of all the possible sequences n bases long.

38.   A device according to paragraph 37, wherein the substantial fraction is any of or range between any two of 25%, 30%, 3.5%, 40%, 45% 50%, 55%, 60%, 65%, 70%, 75%, 80%, 82%, 84%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or more than 99%, substantially all and all.